

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,685

DATE: 01/02/2001
 TIME: 12:08:29

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\01022001\I733685.raw

PS

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3 <110> APPLICANT: Cade, Rebecca M
4   Dietrich, Robert A
6 <120> TITLE OF INVENTION: GENES ENCODING PROTEINS INVOLVED IN THE REGULATION OF
7   SAR GENE EXPRESSION IN PLANTS
9 <130> FILE REFERENCE: A-31089A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/733,685
C--> 12 <141> CURRENT FILING DATE: 2000-12-08
14 <150> PRIOR APPLICATION NUMBER: 60/171,008
15 <151> PRIOR FILING DATE: 1999-12-15
17 <150> PRIOR APPLICATION NUMBER: 60/175,519
18 <151> PRIOR FILING DATE: 2000-01-11
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 509
26 <212> TYPE: DNA
27 <213> ORGANISM: Arabidopsis thaliana
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31 <222> LOCATION: (68)..(433)
32 <223> OTHER INFORMATION: gene product NI16
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: (142)..(147)
37 <223> OTHER INFORMATION: SalI site
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40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (344)..(349)
42 <223> OTHER INFORMATION: EcoRI site
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47 ggclaac atg aac aac tct ttg aag aaa gaa gaa cgc gta gaa gaa gat 109
48   Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp
49       1           5           10
51 aac gga aaa tct gac ggt aac aga ggg aaa ccg tcg acg gaa gtt gtt 157
52 Asn Gly Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val
53   15           20           25           30
55 cgg acg gta acg gag gaa gag gtg gat gag ttt ttc aag ata tta cgg 205
56 Arg Thr Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg
57       35           40           45
59 aga gta cac gtg gcg aca cga acg gtt gcg aaa gtt aac ggc ggt gtt 253
60 Arg Val His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val
61       50           55           60
63 gct gag gga gag tta ccg tct aag aag agg aaa cgg aqt cag aat ctt 301
64 Ala Glu Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Glu Asn Leu
65       65           70           75
67 ggg ttg aga aac tcg ttg gat tgt aac ggc gtt cga gac gga gaa ttc 349

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68 Gly Leu Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe
69      80      85      90
71 gat gag att aat cag qtc ggg tta cag ggt ttg ggt ttg gat ctg aac 397
72 Asp Glu Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn
73 95      100      105      110
75 tgl aaa cag gaa cca gac agc gtt agt tta tcg ttg tagacttgta 443
76 Cys Lys Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
77      115      120
79 gtcttcctatg tttttccccc ttttacaata atcaattttt ttttaactac aatacttttg 503
81 aaaaaa 509
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 122
86 <212> TYPE: PRT
87 <213> ORGANISM: Arabidopsis thaliana
89 <400> SEQUENCE: 2
90 Met Asn Asn Ser Leu Lys Lys Glu Glu Arg Val Glu Glu Asp Asn Gly
91 1      5      10      15
93 Lys Ser Asp Gly Asn Arg Gly Lys Pro Ser Thr Glu Val Val Arg Thr
94      20      25      30
96 Val Thr Glu Glu Glu Val Asp Glu Phe Phe Lys Ile Leu Arg Arg Val
97      35      40      45
99 His Val Ala Thr Arg Thr Val Ala Lys Val Asn Gly Gly Val Ala Glu
100      50      55      60
102 Gly Glu Leu Pro Ser Lys Lys Arg Lys Arg Ser Gln Asn Leu Gly Leu
103 65      70      75      80
105 Arg Asn Ser Leu Asp Cys Asn Gly Val Arg Asp Gly Glu Phe Asp Glu
106      85      90      95
108 Ile Asn Arg Val Gly Leu Gln Gly Leu Gly Leu Asp Leu Asn Cys Lys
109      100      105      110
111 Pro Glu Pro Asp Ser Val Ser Leu Ser Leu
112      115      120
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117 <211> LENGTH: 1700
118 <212> TYPE: DNA
119 <213> ORGANISM: Arabidopsis thaliana
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (365)..(371)
124 <223> OTHER INFORMATION: TCA1 motif
126 <220> FEATURE:
127 <221> NAME/KEY: misc_feature
128 <222> LOCATION: (426)..(435)
129 <223> OTHER INFORMATION: TCA1 motif
131 <220> FEATURE:
132 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (609)..(614)
134 <223> OTHER INFORMATION: MYCATR22 element
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature

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138 <222> LOCATION: (646)..(665)
139 <223> OTHER INFORMATION: CAMV AS1 salicylic acid response element
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153 <222> LOCATION: (863)..(1228)
154 <223> OTHER INFORMATION: NT16 genomic coding region
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158 catgacaaat attaatatat cagtgttaat aacatgtttt gttcttataaa tacatgcatt 120
159 ttaaaatcag acatttgttt taaaatcaaa tetaatctct tatatcaaaa cgacattgac 180
160 qgaaaattca qgtaaaaaga gaaaataaag aatgagagat agagagattt ctatggaaga 240
161 agaaaagagag aacatgttaqg tgaacaaaat aaagagatat gatgatalat ttatlgagag 300
162 qtgttgaaag ttatttttag agagggagag agaaatagaa aaagaaaatg acatggtgaa 360
163 tctgaagaag attgaattgtg ttaaaagfga agagagaaag agaactccat ggcataaagt 420
164 tctgaagaag gatgaaaaag aaaaataaag aqgaagaaga aaagagaaag ctaaaataga 480
165 ctactatttg ccaaaatttc tgtagccgac aaatactatt tggccaagy ttattttgtg 540
166 tatttttttg aagtcataag ttatttctta cataactctt aaaaatataq cggataccaa 600
167 tttttccaca catggacttc ctttattcca aaagtcaata aagtgtagcg tcatgatact 660
168 taccgtttta aacatgcgat gatgatgta tttagatcaa tctccaccgt ccaatttatt 720
169 tagttgttga caatatcgac cgtctaagtt ccacaccgac ggcataaaga gtttcattat 780
170 aaatttttagc aaaaataaat cagcaataaa ttttttcttg actaagctta aacgacgcgc 840
171 ttaacattttt cttctggcta acatgaacaa ctctttgaag aaagaagaac ggcataaaga 900
172 agataacqga aaatctgagc gtaacagagg gaaaccgtcg acggaagttg ttcggacggt 960
173 aacggaqga gagggtgagc agtttttcaa gatattacag aagatcacag tggcgacacg 1020
174 aacgggttgcg aaagttaacg gcggtgttgc tgaggagagc ttaccgtcta agagagagaa 1080
175 acggagtcag aatcttgggt tgagaaacgc gttggattgt aacggcgctc gagacgga 1140
176 attcgatgag attaatcggt tcgggttaca ggggttgggt ttggatctga actgtaaac 1200
177 ggaaccagac agcgttaagt tatcgttgta gaettgtagt ccttcattgt tttcccttc 1260
178 ttacaataat caattttttt ttaactacaa tacttttgaa aaaaatggta aaagaagatt 1320
179 attaacatgt tatccaaatt tcagattctt cagttttatt ttalacgtca aaagagaagt 1380
180 tatatatttg caaaactaca agtcaaacaa angctattta agcgtttgac gttcctaacc 1440
181 aacataaatt ttactaaat caatgtttta aaaaagtgtt gatgtaaaag atatcaattg 1500
182 ggcctttgcc tggcccggtt agtaaatatt cagagtaggt atgggcctgt ataaggaggt 1560
183 ccaaaaaaag agcgggcatt gcgggttggg tgcgtttgga actttggatt gtggattagt 1620
184 catggtttat ctattaatgt ctgcggactt gtggaacgac cgtttgttct tcttctctg 1680
185 tttaagactt acgaacatat 1700
188 <210> SEQ ID NO: 1
189 <211> LENGTH: 608
190 <212> TYPE: DNA
191 <213> ORGANISM: Solanum tuberosum
193 <220> FEATURE:

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194 <221> NAME/KEY: CDS
195 <222> LOCATION: (124)..(438)
197 <400> SEQUENCE: 1
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200 tgaagagaata aagagaagta attgcactag cagtattgac aattaatcag ctageccggt 120
202 tga atg cta ctt atg gac gga gaa aag aag agg aag aga aca gca atc 168
203 Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile
204 1 5 10 15
206 ggc gcc gga gat cgg agt aag gat jag qta gaa gct act gtg aag gag 216
207 Gly Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu
208 20 25 30
210 gag gag ccg ccg tca gag cgg gag gti qac gag ttc ttc gcg atc tta 264
211 Glu Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Ile Leu
212 35 40 45
214 cgg agg atg cat gtg cgg gtg aaa tat ctc caq aga aat gct cag att 312
215 Arg Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile
216 50 55 60
218 cgg ccg gaa aac ctt aac gca tcg ccg gcc ggt gct aac ggt gtc gca 360
219 Arg Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala
220 65 70 75
222 gct gga cgg aag aga gaa cgg gga atc gtg aga aca ggt gat ttg gac 408
223 Ala Gly Arg Lys Arg Glu Arg Gly Tle Val Arg Lys Gly Asp Leu Asp
224 80 85 90 95
226 ctc aac act ctg ccg gac ggc gga gac taa ttaacgcagt ttaagcatag 458
227 Leu Asn Thr Leu Pro Asp Gly Gly Asp
W--> 228 100 105
230 gtttaattaca taaatgcacc cttaattatc qtagattcct aagattgac tgcctacacg 518
232 attaatattat tauagccttt ttttatatat atttctccg taaacgggtt gctctttgtg 578
234 attttcttta ataaatttaa tttattttat 608
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 104
239 <212> TYPE: PRT
240 <213> ORGANISM: Solanum tuberosum
242 <400> SEQUENCE: 5
243 Met Leu Leu Met Asp Gly Glu Lys Lys Arg Lys Arg Thr Ala Ile Gly
244 1 5 10 15
245 Ala Gly Asp Arg Ser Lys Asp Glu Val Glu Ala Thr Val Lys Glu Glu
246 20 25 30
247 Glu Pro Pro Ser Glu Ala Glu Val Asp Glu Phe Phe Ala Tle Leu Arg
248 35 40 45
249 Arg Met His Val Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Arg
250 50 55 60
251 Pro Glu Asn Leu Asn Ala Ser Pro Ala Gly Ala Asn Gly Val Ala Ala
252 65 70 75 80
253 Gly Arg Lys Arg Glu Arg Gly Tle Val Arg Lys Gly Asp Leu Asp Leu
254 85 90 95
255 Asn Thr Leu Pro Asp Gly Gly Asp
256 100
260 <210> SEQ ID NO: 6

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RAW SEQUENCE LISTING
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261 <211> LENGTH: 340
262 <212> TYPE: DNA
263 <213> ORGANISM: Lycopersicon esculentum
264 <220> FEATURE:
265 <221> NAME/KEY: CDS
266 <222> LOCATION: (3)..(233)
269 <400> SEQUENCE: 6
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271 Ser Glu Gly Glu Val Asp Glu Phe Phe Ala Ile Leu Arg Arg Met
272 1 5 10 15
273 cac atg gcc gta aaa tat ctt caa aca aac gct cag att cag ccg gaa 95
274 His Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Gln Pro Glu
275 20 25 30
276 aac gtt aac gct cag gcc agc aag tta acc gca tcc ccg gcc ggt gtt 143
277 Asn Val Asn Ala His Gly Ser Lys Leu thr Ala Ser Pro Ala Gly Val
278 35 40 45
279 aac gga qat gca act gga cag aag aca gaa ccg gga atc gtg aga aaa 191
280 Asn Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly ile Val Arg Lys
281 50 55 60
282 ggt qat tta gac ctc aac act tta ccg gac taa gga gac taa 233
283 Gly Asp Leu Asp Leu Asn Thr Leu Pro Asp Cys Gly Asp
284 65 70 75
285 cgcagtttaa gcatagatta attacagaaa tgcaccttta attatcgtaa attctttaaga 293
286 ttgatctgcl gtacaaatta attaaatgaa gccttttttt atataaaaa aaaaaa 349
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 76
297 <212> TYPE: PRT
298 <213> ORGANISM: Lycopersicon esculentum
300 <400> SEQUENCE: 7
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302 1 5 10 15
303 Met Ala Val Lys Tyr Leu Gln Arg Asn Ala Gln Ile Gln Pro Glu Asn
304 20 25 30
305 Val Asn Ala His Gly Ser Lys Leu Thr Ala Ser Pro Ala Gly Val Asn
306 35 40 45
307 Gly Asp Ala Thr Gly Gln Lys Arg Glu Arg Gly Ile Val Arg Lys Gly
308 50 55 60
309 Asp Leu Asp Leu Asn Thr Leu Pro Asp Cys Gly Asp
310 65 70 75
314 <210> SEQ ID NO: 8
315 <211> LENGTH: 75
316 <212> TYPE: PRT
317 <213> ORGANISM: Glycine max
319 <400> SEQUENCE: 8
320 Met Glu Val Glu Lys Arg Lys Asn Lys Arg Val Met Gly Glu Glu Glu
321 1 5 10 15
322 Glu Ser Glu Arg Val Lys Asn Lys Arg Leu Lys Gly Val Glu Glu Glu
323 20 25 30
324 Asp Gly Ser Asp Gly Val Pro Thr Glu Glu Val Glu Glu Phe Phe

```

TYL

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:530 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:537 M:283 W: Missing Blank Line separator, <220> field identifier